

Fig. 1

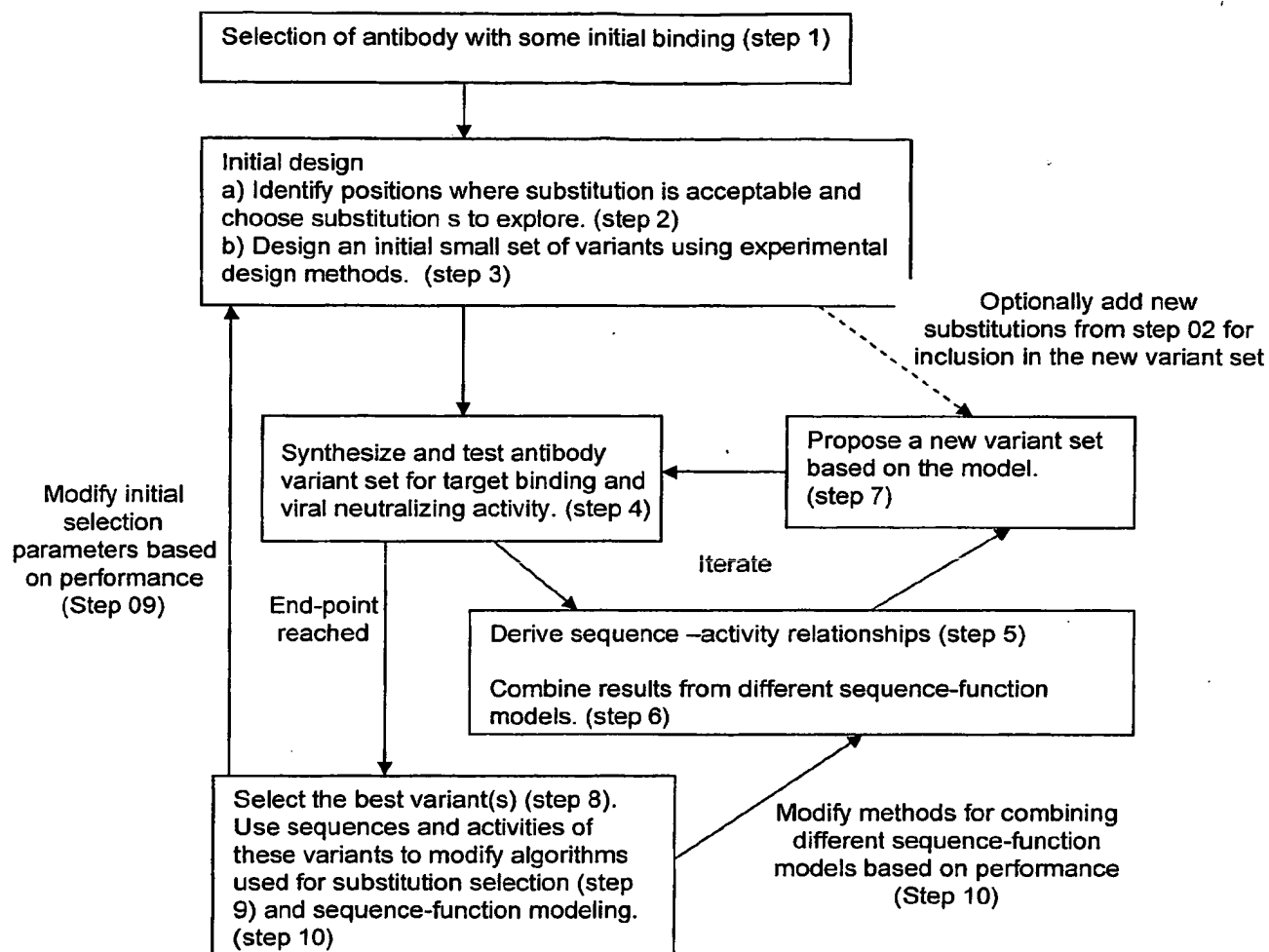


Figure 2

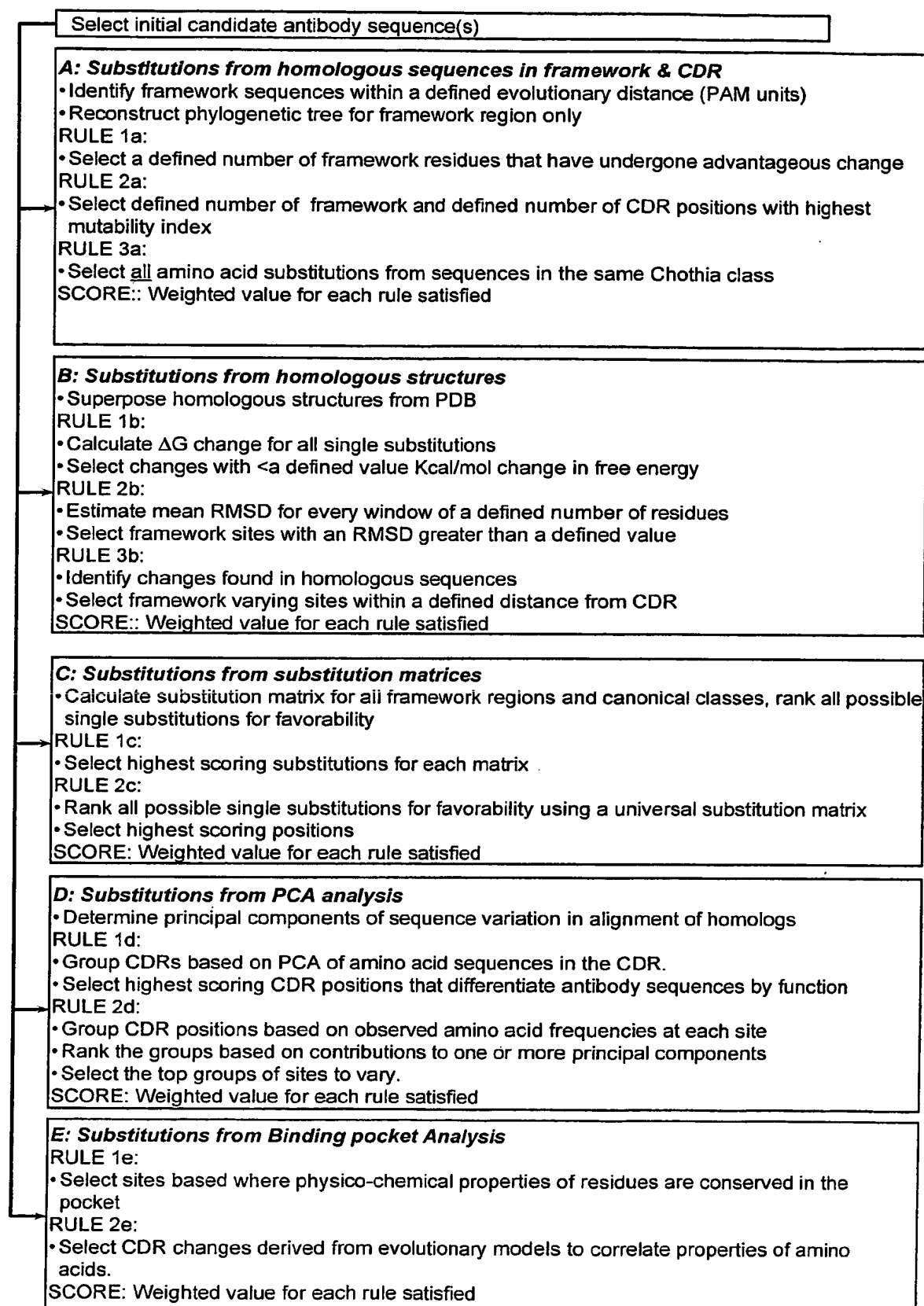
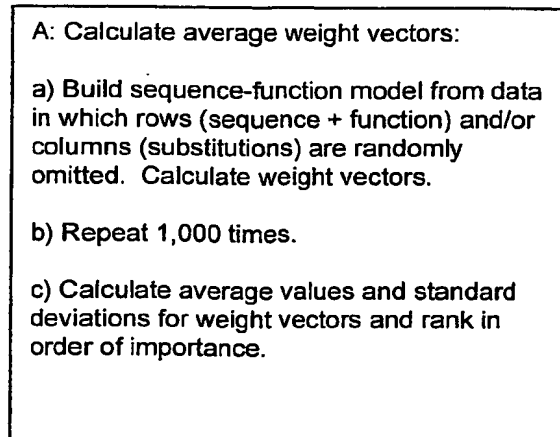
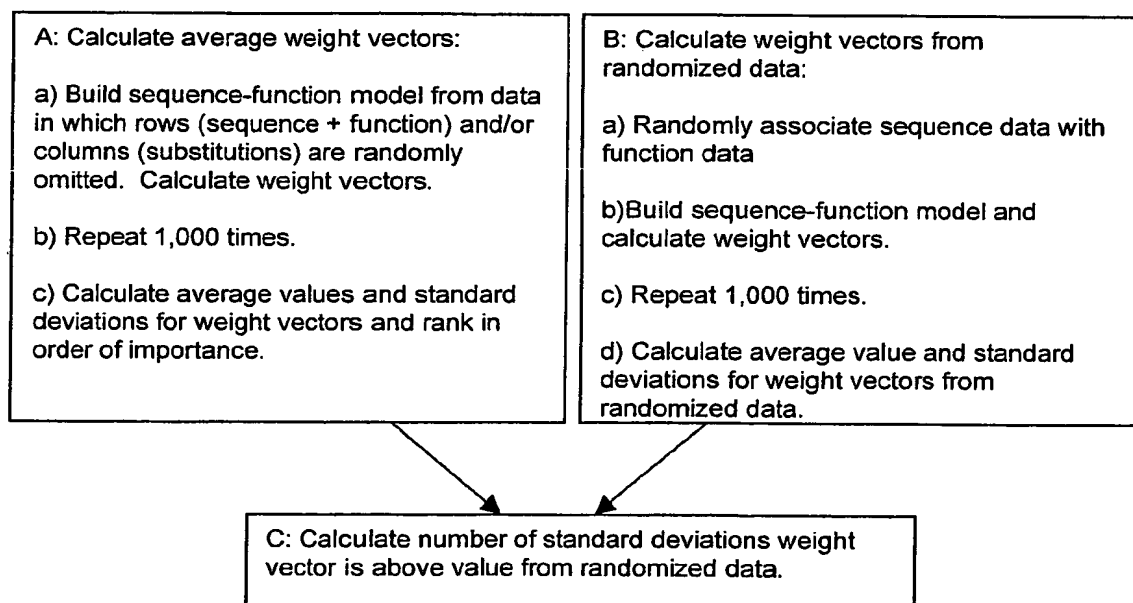


Figure 3

**Figure 4****Figure 5**

E coli leader peptide
 -20 -10 -1
 MKKLLFAIPL VVPFYSHSTM (SEQ ID NO.: 1)

Proteinase K

1	11	21	31	41
APAVEQRSEA	APLIEARGEM	VANKYIVKFK	EGSALSALDA	AMEKISGKPD
51	61	71	81	91
HVYKNVFSGF	AATLDENMVR	VLRAHPDVEY	IEQDAVVTIN	AAQTNAPWGL
101	111	121	131	141
ARISSTSPGT	STYYYDESAG	QGSCVYVIDT	GIEASHPEFE	GRAQMVKTTY
151	161	171	181	191
YSSRDGNGHG	THCAGTVGSR	TYGVAKKTQL	FGVKVLDNDG	SGQYSTIIAG
201	211	221	231	241
MDFVASDKNN	RNCPKGVVAS	LSLGGGYSSS	VNSAAARLQS	SGVMVAVAAG
251	261	271	281	291
NNNADARNYS	PASEPSVCTV	GASDRYDRRS	SFSNYGSVLD	IFGPGTSILS
301	311	321	331	341
TWIGGSTRSI	SGTSMATPHV	AGLAAYLMTL	GKTTAASACR	YIADTANKGD
351	361	371		
LSNIPFGTVN	LLAYNNYQAV	DHHHHHHH	(SEQ ID NO.: 2)	

Figure 6

-60	-50	-40	-30	-20	-10	-1
atgaaaaaac	tgctgttcgc	gattccgctg	gtggtgccgt	tctatagcca	tagcaccatg	
1	11	21	31	41	51	
GCACCGGCCG	TTGAACAGCG	TTCTGAAGCA	GCTCCTCTGA	TTGAGGCACG	TGGTGAAATG	
61	71	81	91	101	111	
GTAGCAAACA	AGTACATCGT	GAAGTTCAAG	GAGGGTTCTG	CTCTGTCTGC	TCTGGATGCT	
121	131	141	151	161	171	
GCTATGGAAA	AGATCTCTGG	CAAGCCTGAT	CACGTCTATA	AGAACGTGTT	CAGCGGTTTC	
181	191	201	211	221	231	
GCAGCAACTC	TGGACGAGAA	CATGGTCCGT	GTACTGCGTG	CTCATCCAGA	CGTTGAATAC	
241	251	261	271	281	291	
ATCGAACAGG	ACGCTGTGGT	TACTATCAAC	GCGGCACAGA	CTAACGCACC	TTGGGGTCTG	
301	311	321	331	341	351	
GCACGTATTT	CTTCTACTTC	CCCGGGTACG	TCTACTTACT	ACTACGACGA	GTCTGCCGGT	
361	371	381	391	401	411	
CAAGGTTCTT	GCGTTTACGT	GATCGATACG	GGCATCGAGG	CTTCTCATCC	TGAGTTTGAA	
421	431	441	451	461	471	
GGCCGTGCAC	AAATGGTGAA	GACCTACTAC	TACTCTTCCC	GTGACGGTAA	TGGTCACGGT	
481	491	501	511	521	531	
ACTCATTGCG	CAGGTACTGT	TGGTAGCCGT	ACCTACGGTG	TTGCTAAGAA	AACGCAACTG	
541	551	561	571	581	591	
TTCGGCGTTA	AAGTGCTGGA	CGACAACGGT	TCTGGTCAGT	ACTCCACCAT	TATCGCGGGT	
601	611	621	631	641	651	
ATGGATTTCG	TAGCGAGCGA	TAAAAACAAC	CGCAACTGCC	CGAAAGGTGT	TGTGGCTTCT	
661	671	681	691	701	711	
CTGTCTCTGG	GTGGTGGETA	CTCCTCTTCT	GTTAACAGCG	CAGCTGCACG	TCTGCAATCT	
721	731	741	751	761	771	
TCCGGTGTCA	TGGTCGCAGT	AGCAGCTGGT	AACAATAACG	CTGATGCACG	CAACTACTCT	
781	791	801	811	821	831	
CCTGCTAGCG	AGCCTTCTGT	TTGCACCGTG	GGTGCATCTG	ATCGTTATGA	TCGTCGTAGC	
841	851	861	871	881	891	
TCCTTCAGCA	ACTATGGTTC	CGTCCTGGAT	ATCTTCGGCC	CTGGTACTTC	TATCCTGTCT	

Figure 7A

901	911	921	931	941	951
ACCTGGATTG	GCGGTAGCAC	TCGTTCCATT	TCCGGTACGA	GCATGGCTAC	TCCACATGTT
961	971	981	991	1001	1011
GCTGGTCTGG	CAGCATACCT	GATGACCCTG	GGTAAGACCA	CTGCTGCATC	CGCTTGTCGT
1021	1031	1041	1051	1061	1071
TACATCGCGG	ATACTGCGAA	CAAAGGCGAT	CTGTCTAACA	TCCCGTTCGG	CACCGTTAAT
1081	1091	1101	1111	1121	1131
CTGCTGGCAT	ACAACAATA	TCAGGCTgtc	gaccatcatc	atcatcatca	tag

(SEQ ID NO.: 3)

Figure 7B

gi|19171215|emb|CAD20578.1|/89
gi|19171217|emb|CAD20579.1|/1-
gi|19171219|emb|CAD20580.1|/1-
gi|19171221|emb|CAD20581.1|/1-
gi|16215662|emb|CAC95042.1|/90
gi|16506136|dbj|BAB70705.1|/78
gi|16506134|dbj|BAB70704.1|/78
gi|16506140|dbj|BAB70707.1|/78
gi|16215677|emb|CAC95049.1|/90
gi|117631|sp|P29138|CUDP_METAN
gi|6624958|emb|CAB63911.1|/90-
gi|16215669|emb|CAC95045.1|/90
gi|460032|gb|AAA91584.1|/84-36
gi|6634475|emb|CAB64346.1|/87-
gi|16215664|emb|CAC95043.1|/87
gi|2351388|gb|AAC49831.1|/86-3
gi|8671180|emb|CAB95012.1|/85-
gi|16215666|emb|CAC95044.1|/85
gi|16215671|emb|CAC95046.1|/85
gi|4092486|gb|AAC99421.1|/64-2
gi|18542429|gb|AAL75579.1|AF46
SUTIKA/91-367
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gi|230675|pdb|2PRK|/1-277
gi|494434|pdb|1PEK|E/1-277
gi|224977|prf||1205229A/1-275
gi|14278658|pdb|1IC6|A/1-277
gi|131084|sp|P23653|PRTR_TRIAL
gi|4761119|gb|AAD29255.1|AF104
gi|14626933|gb|AAK70804.1|/81-
gi|639712|gb|AAC48979.1|/83-34
gi|742825|prf||2011184A/84-362
gi|628051|pir||JC2142/84-362
gi|15808791|gb|AAL08502.1|AF41
gi|15808805|gb|AAL08509.1|AF41
gi|28918475|gb|EAA28148.1|/90-
gi|10181226|gb|AAC27316.2|/92-
gi|131088|sp|P20015|PRTT_TRIAL
gi|9971109|emb|CAC07219.1|/86-
gi|7543916|emb|CAB87194.1|/89-
gi|5813790|gb|AAD52013.1|AF082
gi|23894244|emb|CAD23614.1|/11
gi|22652141|gb|AAN03634.1|AF40
gi|24528136|emb|CAD24010.1|/10
gi|24528132|emb|CAD24008.1|/10
A35742./126-403
gi|114081|sp|P08594|AQL1_THEAQ
AAA82980./129-408
gi|15640187|ref|NP_229814.1|/1
AAA22247./107-381

Figure 8

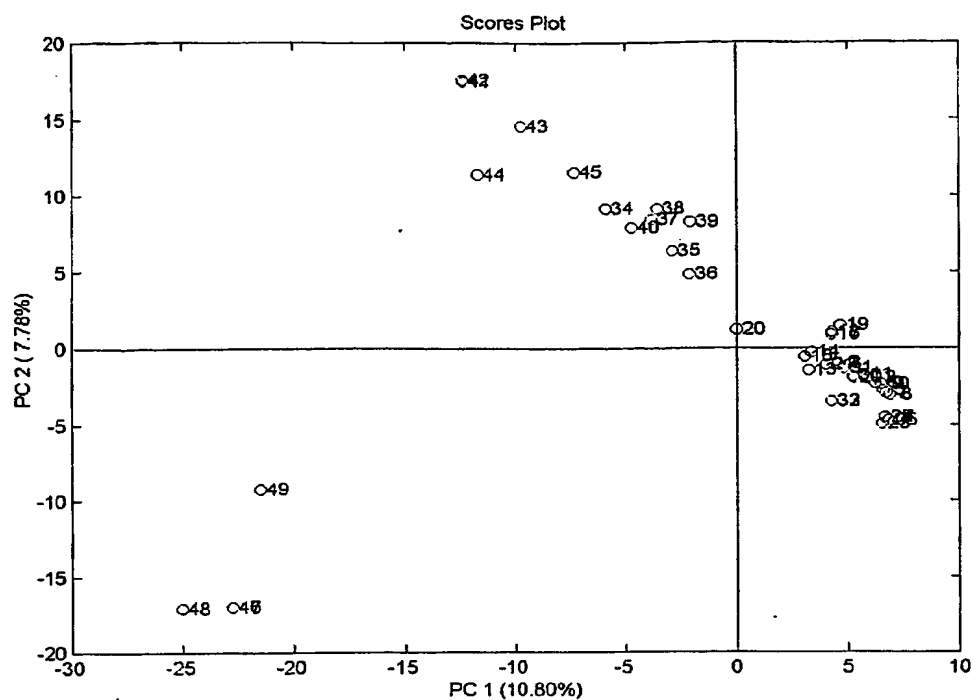


Figure 9

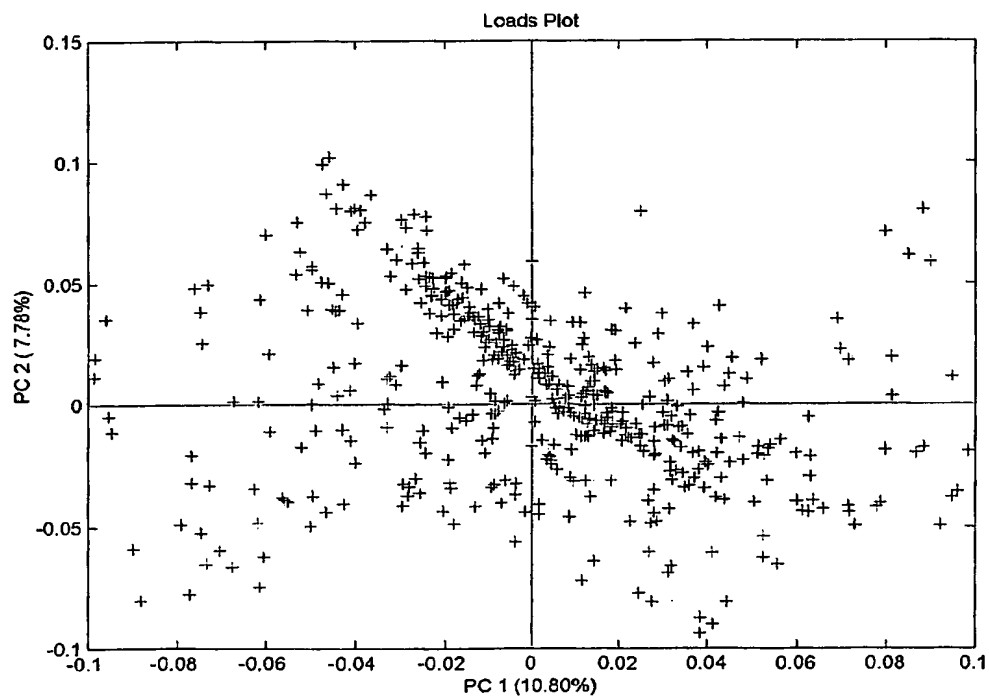


Figure 10

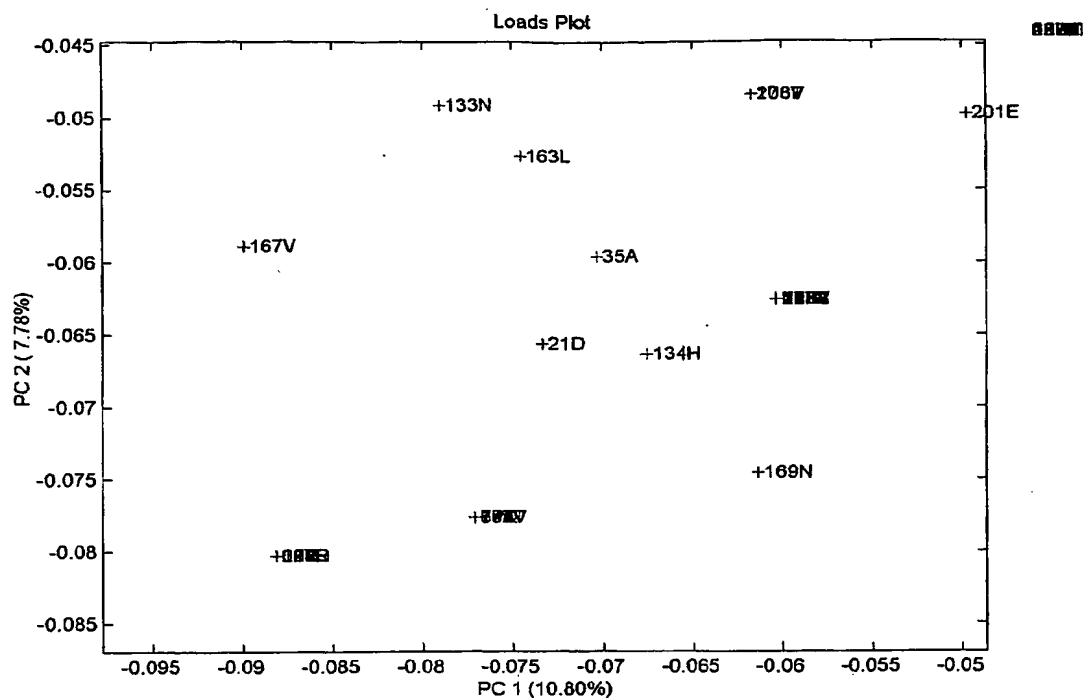


Figure 11

Residue	PC1 contrib.	PC2 contrib.	PC1+2 contrib.
15D	-0.0881	-0.0803	-0.1684
18D	-0.0881	-0.0803	-0.1684
19Q	-0.0881	-0.0803	-0.1684
22L	-0.0881	-0.0803	-0.1684
23P	-0.0881	-0.0803	-0.1684
65Y	-0.0881	-0.0803	-0.1684
66D	-0.0881	-0.0803	-0.1684
110R	-0.0881	-0.0803	-0.1684
137P	-0.0881	-0.0803	-0.1684
164D	-0.0881	-0.0803	-0.1684
189C	-0.0881	-0.0803	-0.1684
198R	-0.0881	-0.0803	-0.1684
8P	-0.0772	-0.0777	-0.1549
34T	-0.0772	-0.0777	-0.1549
67A	-0.0772	-0.0777	-0.1549
75Q	-0.0772	-0.0777	-0.1549
161T	-0.0772	-0.0777	-0.1549
199V	-0.0772	-0.0777	-0.1549
167V	-0.0899	-0.0589	-0.1488
21D	-0.0733	-0.0657	-0.1390
169N	-0.0613	-0.0746	-0.1359
134H	-0.0675	-0.0664	-0.1339

Figure 12

VariationScore		Primary contribution to score
N95C	5	Structural stability at higher temperature: from published literature
P97S	3	P to S for flexibility and structural perturbabtion
S107D	5	from active homologs
S123A	7	Thermostable consensus
E138A	5	From experiments in literature
M145F	5	From experiments to improve thermostability
Y151A	8	From experiments to improve thermostability
V167I	10	Allow user specified conservative changes (controlled perturbation)
L180I	10	Allow user specified conservative changes (controlled perturbation)
Y194S	10	Varaiaion observed in highly active clone from our initial exp.
A199S	8	Allow user specified conservative changes (controlled perturbation)
K208H	7	PCA modelling of homologs collected from GenBank.
A236V	7	PCA modelling of homologs collected from GenBank.
R237N	5	From experiments to improve thermostability (in literature)
P265S	3	P to S for flexibility and structural perturbabtion
V267I	10	Allow user specified conservative changes (controlled perturbation)
S273T	15	Multiple sources identify this change. (thermostability and other)
G293A	8	For thermostability considerations (observed in thermitases)
L299C	5	For disulphide bridges with N95C (from literature)
I310K	5	from structural studies
K332R	8	for thermostability considerations (observed in thermitases)
S337N	8	for thermostability considerations (observed in thermitases)
P355S	3	P to S for flexibility and structural perturbabtion

Figure 13

variant-1: 123, 151, 293, 310, 332, 355
variant-2: 95, 145, 167, 199, 237, 273
variant-3: 97, 138, 180, 194, 236, 267
variant-4: 107, 132, 208, 265, 299, 337
variant-5: 123, 145, 151, 167, 273, 337
variant-6: 97, 107, 180, 236, 237, 310
variant-7: 123, 138, 199, 208, 265, 355
variant-8: 95, 194, 267, 293, 299, 332
variant-9: 95, 132, 138, 145, 167, 208
variant-10: 236, 237, 273, 293, 332, 355
variant-11: 97, 123, 265, 299, 310, 337
variant-12: 107, 151, 180, 194, 199, 267
variant-13: 95, 107, 123, 180, 194, 337
variant-14: 138, 151, 167, 199, 208, 299
variant-15: 97, 145, 237, 273, 293, 310
variant-16: 132, 236, 265, 267, 332, 355
variant-17: 97, 151, 199, 236, 299, 355
variant-18: 95, 107, 167, 180, 293, 310
variant-19: 145, 237, 265, 267, 332, 337
variant-20: 123, 132, 138, 194, 208, 273
variant-21: 123, 208, 236, 267, 293, 299
variant-22: 107, 132, 138, 145, 337, 355
variant-23: 97, 180, 194, 199, 265, 310
variant-24: 95, 151, 167, 237, 273, 332

Figure 14

Variant #	Changes	Reasons
variant-25	95	Confirm detrimental effect on enzyme
variant-26	97	Confirm detrimental effect on enzyme
variant-27	138	Confirm detrimental effect on enzyme
variant-28	208	Confirm detrimental effect on enzyme
variant-29	236	Confirm detrimental effect on enzyme
variant-30	237	Confirm detrimental effect on enzyme
variant-31	265	Confirm detrimental effect on enzyme
variant-32	299	Confirm detrimental effect on enzyme
variant-33	107, 123, 145	New combinations of positive changes
variant-34	151, 167, 180	New combinations of positive changes
variant-35	194, 199, 267	New combinations of positive changes
variant-36	273, 293, 310	New combinations of positive changes
variant-37	332, 337, 355	New combinations of positive changes
variant-38	107, 151, 194, 273, 332	New combinations of positive changes
variant-39	123, 167, 199, 293, 337	New combinations of positive changes
variant-40	145, 180, 267, 310, 355	New combinations of positive changes
variant-41	107, 167, 267, 273, 337	New combinations of positive changes
variant-42	123, 180, 194, 293, 355	New combinations of positive changes
variant-43	145, 151, 199, 310, 332	New combinations of positive changes
variant-44	145, 167, 194	New combinations of positive changes
variant-45	180, 199, 273	New combinations of positive changes
variant-46	267, 293, 332	New combinations of positive changes
variant-47	310, 337, 107	New combinations of positive changes
variant-48	355, 123, 151	New combinations of positive changes

Figure 15

Sequence changes			Variants																	
Position	WT	Mut	10	12	13	14	15	19	20	21	22	23	24	25	26	27	29	30	31	
25	Y	H											H							
34	A	S													S					
48	K	E																		
50	D	N								N										
55	N	S												S						
63	T	S																		
88	T	I																		
95	N	C																		
97	P	S																		
107	S	D				D												D	D	
123	S	A		A																
132	I	V			V															
138	E	A																		
145	M	F			F															
151	Y	A		A	A	A						A	A	A				A	A	
167	V	I			I							I	I	I						
180	L	I				I						I	I	I						
194	Y	S	S			S									S			S	S	
199	A	S				S									S					
208	K	H						H												
209	N	K																		
233	S	N																		
236	A	V																		
237	R	N					N		N	N										
265	P	S									S									
267	V	I				I									I					
273	S	T			T		T									T		T	T	
293	G	A		A			A									A				
299	L	C																		
310	I	K		K												K				
332	K	R		R			R										R	R	R	
337	S	N			N												N			
355	P	S		S			S										S			
362	L	M							M											
363	A	V										V								
369	A	V																		

Figure 16A

Sequence changes			Variants																	
Position	WT	Mut	32	33	35	36	37	38	39	40	41	42	43	45	46	47	48	49	50	
25	Y	H																		
34	A	S																		
48	K	E																		
50	D	N																		
55	N	S																		
63	T	S																		
88	T	I														I				
95	N	C																		
97	P	S																		
107	S	D			D							D								
123	S	A	A	A		A	A						A							
132	I	V																		
138	E	A																		
145	M	F						F												
151	Y	A											A			A	A	A	A	
167	V	I	I	I	I			I								I	I	I	I	
180	L	I				I	I		I							I	I	I	I	
194	Y	S				S	S	S												
199	A	S	S	S					S											
208	K	H																		
209	N	K																		
233	S	N																		
236	A	V																		
237	R	N												N	N					
265	P	S																		
267	V	I			I					I	I									
273	S	T			T				T											
293	G	A	A	A		A	A			A	A									
299	L	C																		
310	I	K										K								
332	K	R								R	R									
337	S	N	N	N	N							N								
355	P	S				S	S						S							
362	L	M																		
363	A	V						V												
369	A	V												V						

Figure 16B

Sequence changes			Variants											
Position	WT	Mut	N2	N3	N4	N6	N7	N8	N9	N10	N11	N13	N14	N15
25	Y	H												
34	A	S												
48	K	E												
50	D	N												
55	N	S												
63	T	S												
88	T	I												
95	N	C	C					C	C			C		
97	P	S		S		S					S			S
107	S	D			D	D						D		
123	S	A					A				A	A		
132	I	V			V				V					
138	E	A		A			A		A				A	
145	M	F	F						F					F
151	Y	A											A	
167	V	I	I						I				I	
180	L	I		I		I						I		
194	Y	S		S				S				S		
199	A	S	S				S						S	
208	K	H			H		H		H				H	
209	N	K												
233	S	N												
236	A	V		V		V				V				
237	R	N	N			N				N				N
265	P	S			S		S				S			
267	V	I		I				I						
273	S	T	T							T				T
293	G	A						A		A				A
299	L	C			C			C			C		C	
310	I	K				K					K			K
332	K	R						R		R				
337	S	N			N						N	N		
355	P	S					S			S				
362	L	M												
363	A	V												
369	A	V												

Figure 16C

Sequence changes			Variants																
Position	WT	Mut	N16	N17	N18	N19	N20	N21	N22	N23	N24	N25	N26	N27	N28	N30	N33	N40	N43
25	Y	H																	
34	A	S																	
48	K	E																	
50	D	N																	
55	N	S																	
63	T	S																	
88	T	I																	
95	N	C			C						C	C							
97	P	S		S						S			S	S					
107	S	D			D				D								D		
123	S	A					A	A									A		
132	I	V	V				V		V										
138	E	A					A		A						A				
145	M	F				F			F								F	F	F
151	Y	A		A							A								A
167	V	I			I						I								
180	L	I			I					I								I	
194	Y	S					S			S				S					
199	A	S		S						S									S
208	K	H					H	H											
209	N	K																	
233	S	N																	
236	A	V	V	V				V								V			
237	R	N				N					N								
265	P	S	S			S				S									
267	V	I	I			I		I										I	
273	S	T					T				T								
293	G	A			A			A											
299	L	C		C				C					C	C					
310	I	K			K					K								K	K
332	K	R	R			R					R								R
337	S	N				N			N										
355	P	S	S	S					S									S	
362	L	M																	
363	A	V																	
369	A	V																	

Figure 16D

Sequence changes			Variants																
Position	WT	Mut	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63
25	Y	H																	
34	A	S																	
48	K	E																	
50	D	N																	
55	N	S																	
63	T	S																	
88	T	I	I																
95	N	C																	
97	P	S																	
107	S	D																	
123	S	A																	
132	I	V																	
138	E	A																	
145	M	F																	
151	Y	A	A	A	A	A													
167	V	I	I	I	I	I							I	I			I	I	I
180	L	I	I	I	I	I													
194	Y	S					S	S	S	S									
199	A	S					S	S	S	S									
208	K	H									H	H							
209	N	K									K								
233	S	N											N						
236	A	V																	
237	R	N													N	N	N	N	N
265	P	S																	
267	V	I					I	I	I	I	I	I	I	I	I	I			I
273	S	T																	
293	G	A									A	A	A	A	A	A	A	A	A
299	L	C																	
310	I	K																	
332	K	R									R	R	R	R	R	R	R	R	R
337	S	N											N	N					N
355	P	S													S	S	S	S	S
362	L	M																	
363	A	V																	
369	A	V																	

Figure 16E

Sequence changes			Variants															
Position	WT	Mut	65	66	67	69	70	71	72	73	74							
25	Y	H																
34	A	S																
48	K	E						E										
50	D	N																
55	N	S																
63	T	S							S									
88	T	I																
95	N	C																
97	P	S																
107	S	D																
123	S	A																
132	I	V																
138	E	A																
145	M	F																
151	Y	A																
167	V	I	I	I		I	I	I	I									
180	L	I																
194	Y	S																
199	A	S																
208	K	H						H	H	H	H							
209	N	K																
233	S	N																
236	A	V																
237	R	N						N	N									
265	P	S																
267	V	I	I	I	I	I	I	I	I	I	I							
273	S	T				T	T											
293	G	A	A	A				A	A	A	A							
299	L	C																
310	I	K																
332	K	R	R	R	R	R	R	R	R	R	R							
337	S	N			N	N	N	N	N									
355	P	S			S			S	S									
362	L	M																
363	A	V																
369	A	V								V	V							

Figure 16F

Variant	y1	y2	y4	y5	y6	y7
wt	0.7526	0.8774	0.7477	1.1850	0.6604	2
wt	1.2316	1.0877	1.2523	0.8150	1.3396	2
wt	1.0822	0.9082	1.0894	1.0850	0.9829	2
wt	0.8904	1.1423	0.9106	0.9158	1.0171	2
10	0.0263	1.7208	0.1682	-0.0125	0.0453	6
12	0.2211	0.1878	0.4486	0.2320	0.0415	2
13	0.0158	1.9119	0.2430	-0.0376	0.0302	1
14	0.0158	2.3899	0.3364	0.0251	0.0377	6
15	1.6789	0.0135	2.3738	1.6176	0.0226	
15	1.3945	0.4917	1.6260	1.2690	0.6857	
19	0.9000	0.9476	1.0280	1.0219	0.8528	1
19	0.6932	1.0442	0.6667	0.8143	0.7238	1
20	1.2737	0.0593	1.5327	1.5172	0.0755	0
20	0.5507	0.0484	0.5203	0.6472	0.0267	0
21	0.1632	0.9251	0.0935	0.1881	0.1509	0
22	0.1947	0.3294	0.1869	0.2884	0.0642	2
23	1.8053	0.0878	3.0280	2.0000	0.1585	3
23	1.6932	0.0900	2.0163	1.6709	0.1524	3
24	0.0579	0.9777	0.0374	0.0627	0.0566	4
25	0.3421	1.4891	0.6168	0.4514	0.5094	6
26	0.0053	10.7547	0.2056	0.0094	0.0566	2
26	0.0521	0.4391	0.0650	0.0127	0.0229	2
27	0.3474	1.3905	0.3178	0.3793	0.4830	1
29	1.4263	0.0079	1.6822	1.6144	0.0113	4
29	1.2740	0.0150	1.7398	1.3431	0.0190	4
30	0.0316	0.9560	0.0935	-0.0251	0.0302	8
31	0.0421	1.2547	0.1121	0.0502	0.0528	6
32	0.7316	1.2792	0.6916	1.0063	0.9358	4
33	0.3263	1.3530	0.5794	0.5235	0.4415	4
35	1.0737	0.1546	1.7009	1.4451	0.1660	1
36	0.0421	0.9858	0.2617	0.0752	0.0415	2
37	0.0316	0.9560	0.0187	-0.0094	0.0302	2
38	0.0053	9.3208	-0.0748	-0.0157	0.0491	0
39	0.2158	1.2416	0.2430	0.3730	0.2679	1
40	1.6737	1.5444	2.5794	2.0031	2.5849	2
40	0.9342	1.4557	0.9593	0.9666	1.3600	2
41	0.9421	1.8906	1.1402	1.2539	1.7811	2
42	0.0474	1.3543	0.0935	0.0784	0.0642	0
43	0.4105	0.1287	0.5794	0.6364	0.0528	4
43	1.0466	0.0109	0.9919	0.6113	0.0114	4
46	0.4466	1.0919	0.3089	0.5245	0.4876	0.5
47	0.6575	0.7763	0.6016	0.8143	0.5105	7
48	0.9370	0.8253	0.9919	1.1168	0.7733	4
51	0.0219	1.5643	-0.0488	0.0127	0.0343	1
55	1.0329	1.4901	1.0569	1.2986	1.5390	5

Figure 17A

Variant	y1	y2	y4	y5	y6	y7
56	1.3178	1.3124	1.5447	1.3198	1.7295	2
57	1.3123	0.9957	1.3496	1.2986	1.3067	3
58	0.9699	0.4635	0.8943	1.0237	0.4495	2
59	0.5260	0.0435	0.2927	0.5753	0.0229	0.5
60	0.5863	0.0325	0.3740	0.6578	0.0190	0.5
61	0.8548	0.0089	0.9268	0.9137	0.0076	0.5
62	0.3041	0.0752	0.2276	0.3574	0.0229	0.5
63	0.9370	0.0447	0.9919	0.9941	0.0419	0.5
65	0.3699	0.3193	0.0976	0.3955	0.1181	2
66	0.9096	0.5445	0.7480	0.9835	0.4952	2
67	0.2932	0.0520	0.1626	0.3194	0.0152	2
69	0.2301	0.2980	0.1951	0.1713	0.0686	2
70	0.5342	0.3066	0.2927	0.6028	0.1638	3
71	0.2411	0.3002	0.2114	0.2686	0.0724	0.5
72	0.4466	0.0427	0.2276	0.4611	0.0190	1
73	0.2219	0.7725	0.1138	0.2390	0.1714	4
74	0.7233	1.1113	0.4715	0.8164	0.8038	4

Figure 17B

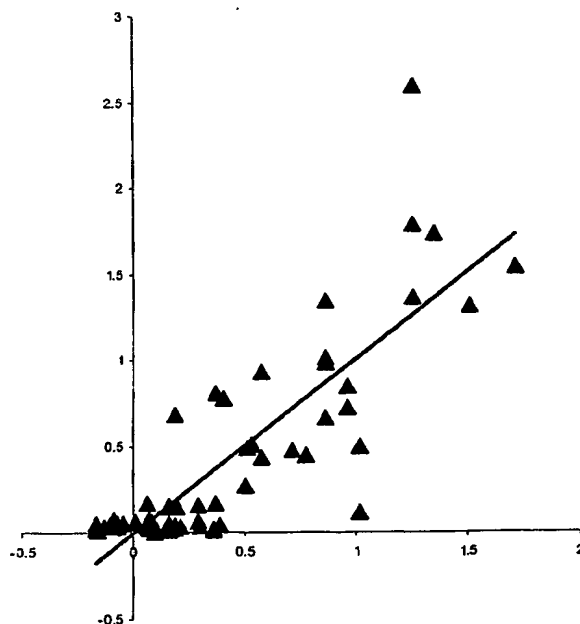


Figure 18

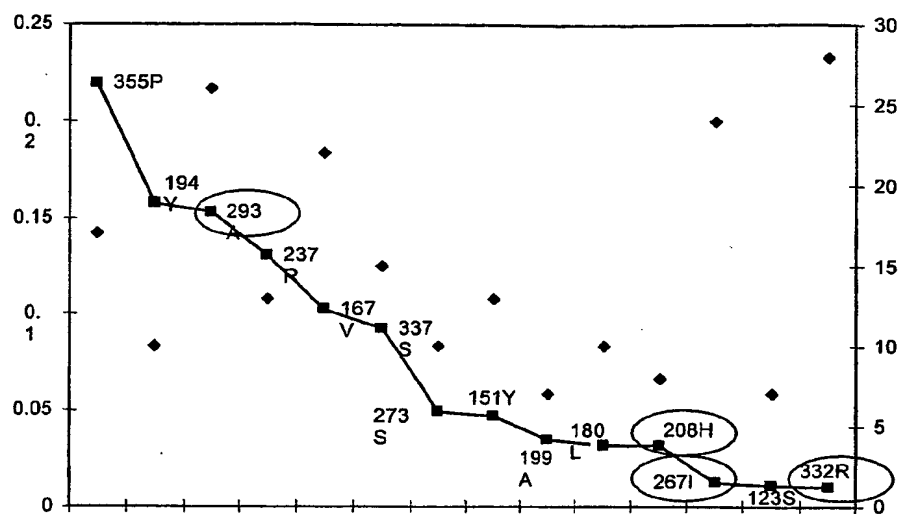


Figure 19

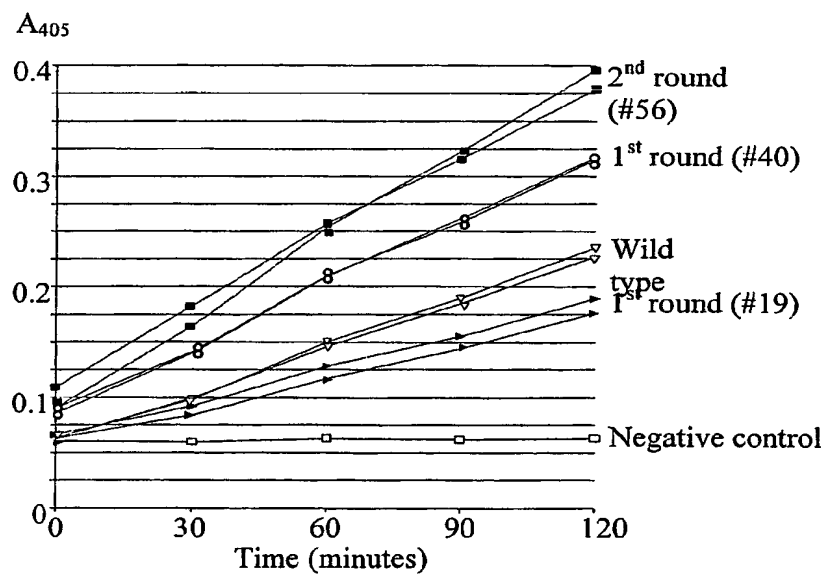


Figure 20

Variation position	Casein hydrolysis (y7)	Thermal tolerance (y6)	AAPL-p-NA pH7.0 (y1)
107	<u>D</u>	S	S
123	<u>A</u>	S	S
151	<u>A</u>	Y	<u>A</u>
167	<u>I</u>	V	V
180	<u>I</u>	L	<u>I</u>
194	<u>S</u>	Y	Y
199	<u>S</u>	A	A
208	K	<u>H</u>	K
267	V	<u>I</u>	V
273	<u>T</u>	S	S
293	G	<u>A</u>	<u>A</u>
332	<u>R</u>	<u>R</u>	<u>R</u>

Figure 21

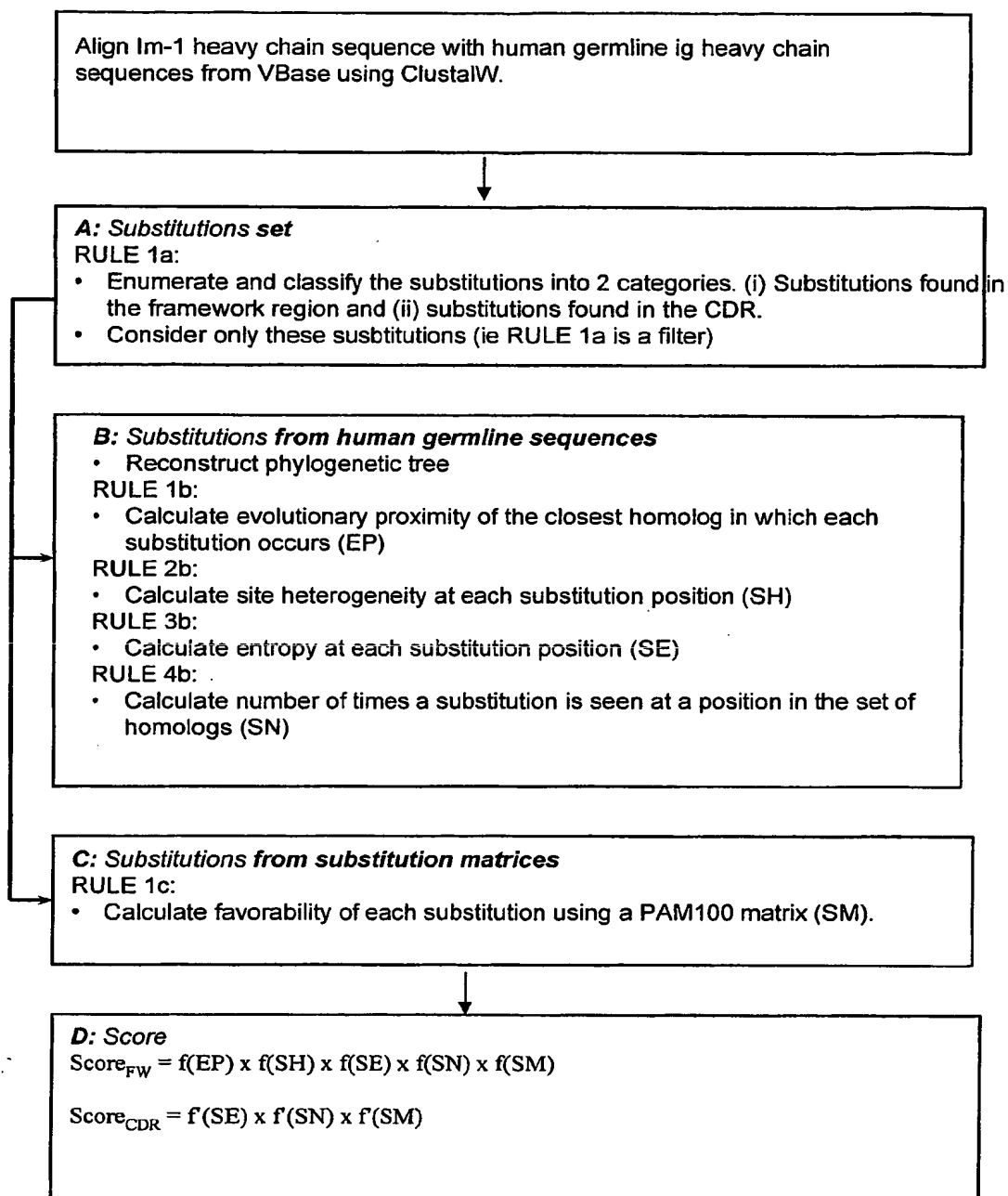


Figure 22

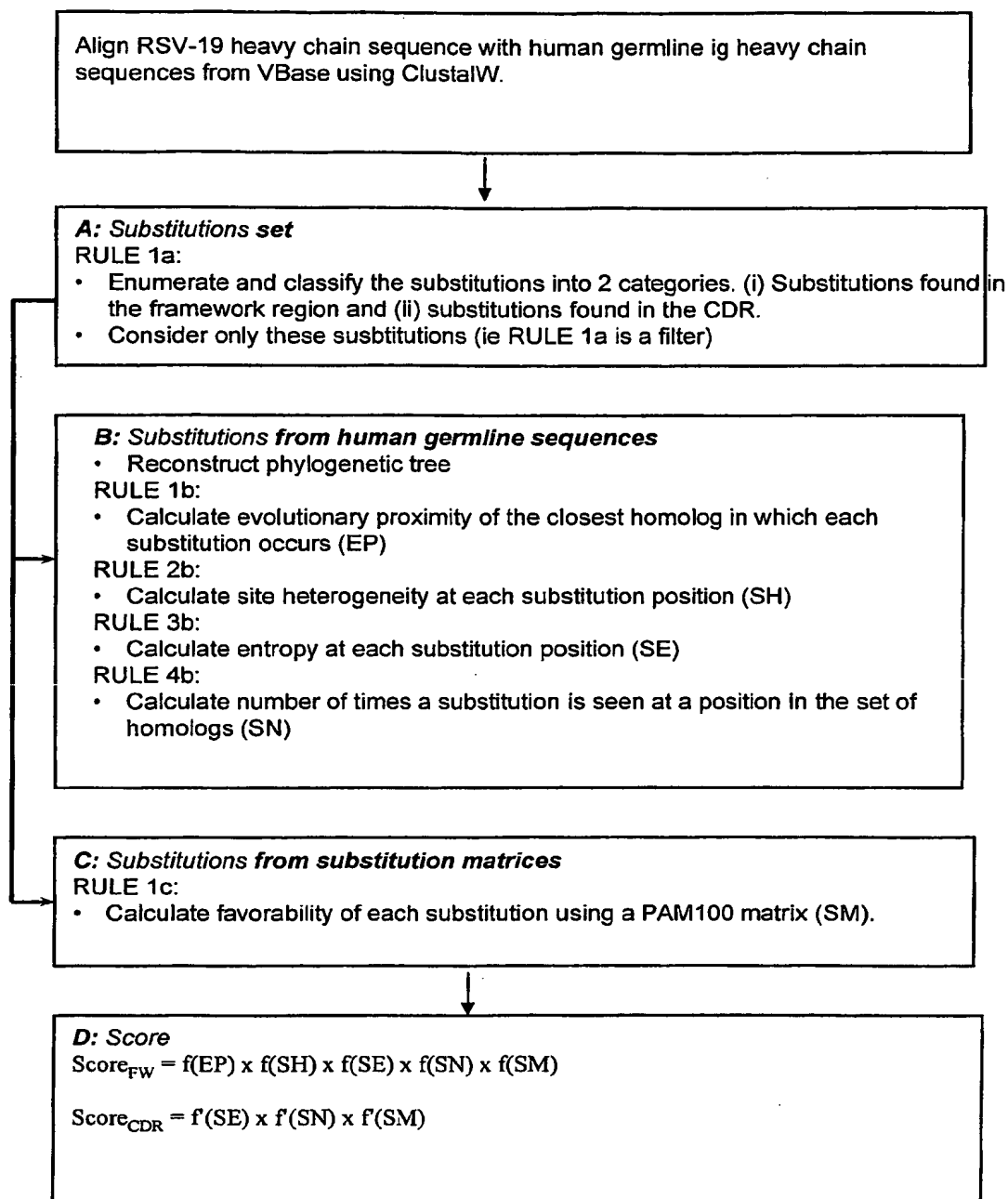


Figure 23

Locus-1-03
Locus-1-08
Locus-1-18
Locus-1-24
Locus-1-45
Locus-1-46
Locus-1-58
Locus-1-69
Locus-1-e
Locus-1-f
Locus-2-26
Locus-2-70
Locus-3-09
Locus-3-11
Locus-3-13
Locus-3-15
Locus-3-20
Locus-3-21
Locus-3-23
Locus-3-30
Locus-3-30.3
Locus-3-30.5
Locus-3-33
Locus-3-43
Locus-3-48
Locus-3-49
Locus-3-53
Locus-3-64
Locus-3-66
Locus-3-72
Locus-3-73
Locus-3-74
Locus-3-d
Locus-4-28
Locus-4-30.1
Locus-4-30.2
Locus-4-30.4
Locus-4-31
Locus-4-34
Locus-4-39
Locus-4-59
Locus-4-61
Locus-4-b
Locus-5-a

Figure 24

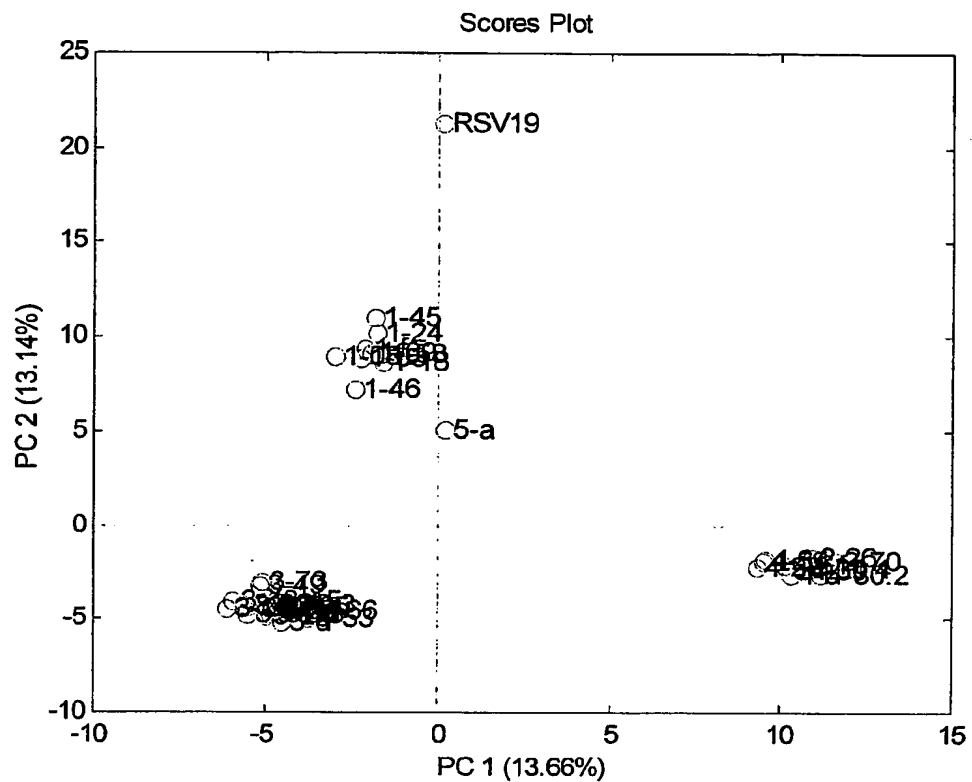


Figure 25

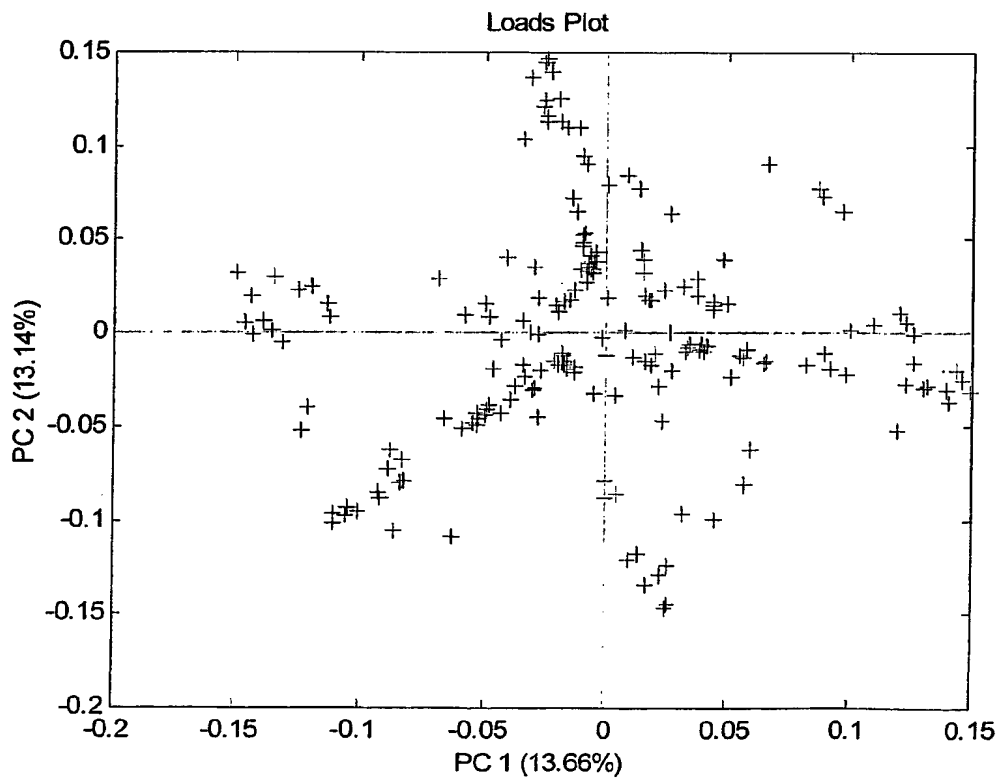


Figure 26

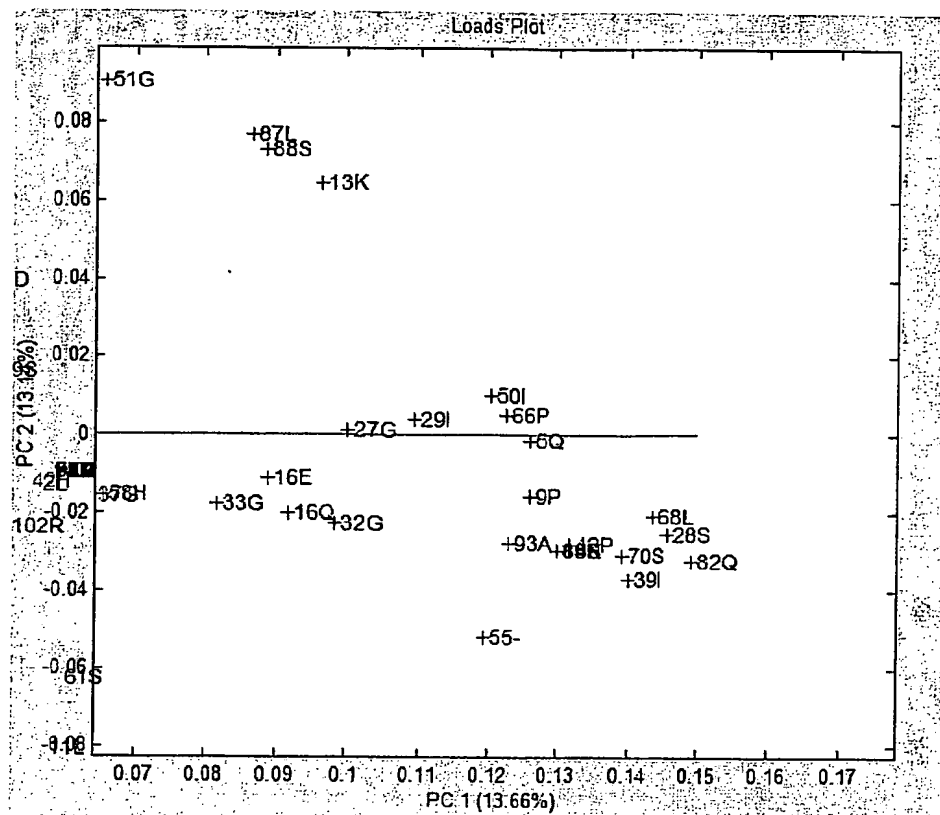


Figure 27

Substitutions	PC1 loads
27G	0.1001
29I	0.1094
50I	0.1204
66P	0.1226
93A	0.1229
5Q	0.1259
9P	0.126
15S	0.13
19S	0.13
65N	0.13
83F	0.13
84S	0.13
86K	0.13
42P	0.1317
70S	0.1392

Figure 28

Locus-1-03
Locus-1-08
Locus-1-18
Locus-1-24
Locus-1-45
Locus-1-46
Locus-1-58
Locus-1-69
Locus-1-e
Locus-1-f
Locus-2-26
Locus-2-70
Locus-3-09
Locus-3-11
Locus-3-13
Locus-3-15
Locus-3-20
Locus-3-21
Locus-3-23
Locus-3-30
Locus-3-30.3
Locus-3-30.5
Locus-3-33
Locus-3-43
Locus-3-48
Locus-3-49
Locus-3-53
Locus-3-64
Locus-3-66
Locus-3-72
Locus-3-73
Locus-3-74
Locus-3-d
Locus-4-28
Locus-4-30.1
Locus-4-30.2
Locus-4-30.4
Locus-4-31
Locus-4-34
Locus-4-39
Locus-4-59
Locus-4-61
Locus-4-b
Locus-5-a

Figure 29

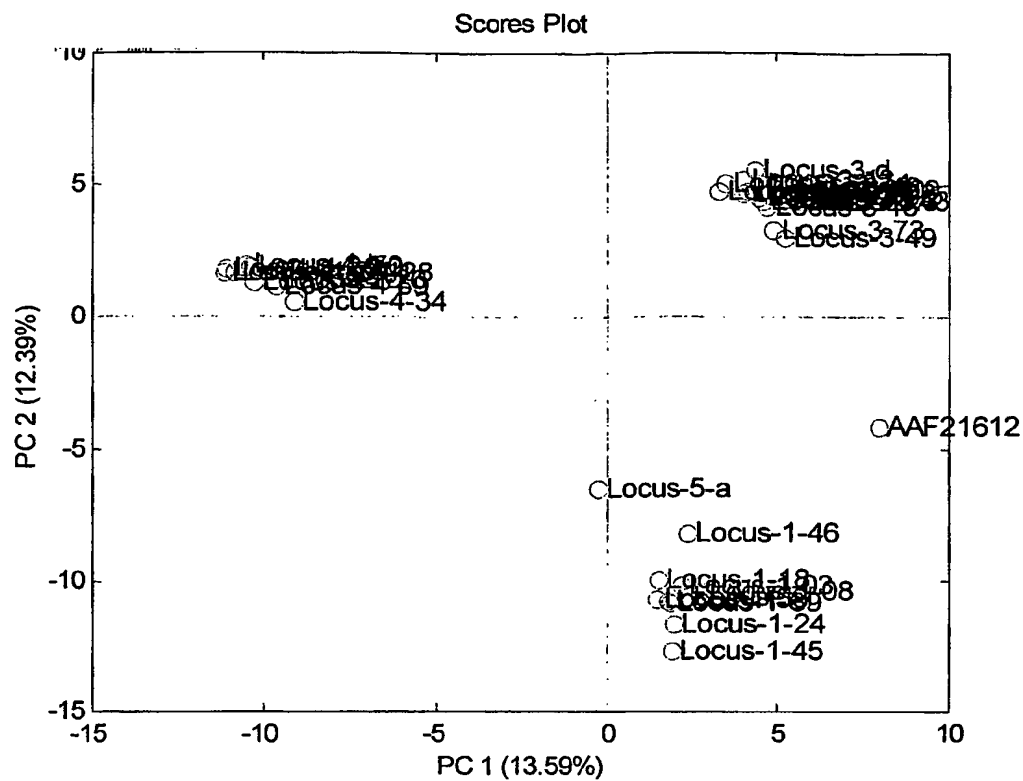


Figure 30

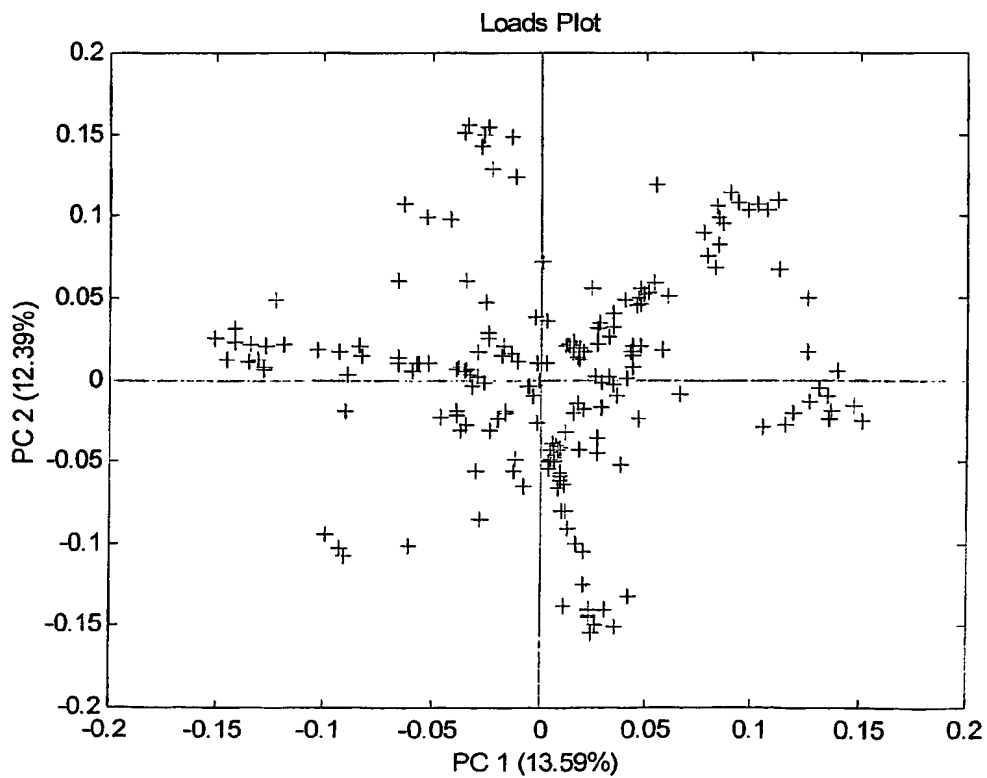


Figure 31

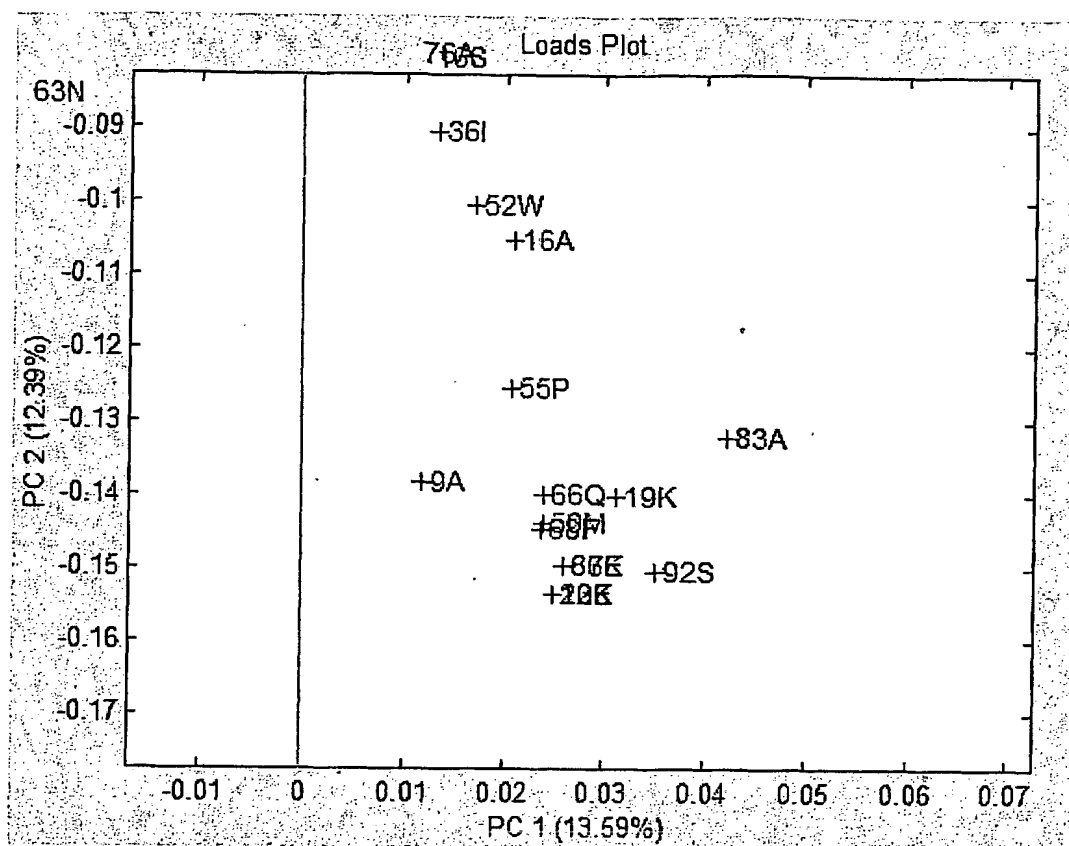


Figure 32

Substitutions	PC1 Loads
82Q	-0.1507
68L	-0.1452
39I	-0.1421
70S	-0.1421
28S	-0.135
5Q	-0.1344
15S	-0.1344
19S	-0.1344
65N	-0.1344
83F	-0.1344
84S	-0.1344
86K	-0.1344
66P	-0.1303
50I	-0.1281
9P	-0.128

Figure 33